

FIGURE 1A

	10	20	30	40	50	60
serotype f	<u>MNQKIVVISSFYMLGAHSFSKAVYHNDRSVKLMKRIDINHQAQRFSIRKYAFGAASVLIG</u>					
serotype c	-----MKRIDINHQAQRFSIRKYAFGAASVLIG					
	70	80	90	100	110	120
serotype f	<u>CVFFLGTQNVSAQEQGTQLPASENAVNVNAENSVVAISQAVADKAATQTTLTETPQVEVEE</u>					
serotype c	<u>CVFFLGTQNVSAQEQGTQLPASENAVNVNAENSVVAISQAVSDKAAAQTTLTETPQVEVEE</u>					
	130	140	150	160	170	180
serotype f	<u>KESKVNAPALNVDDKGAKSSEDVNPTISKTA SEVEASAVTATDTKNSNPQVNVETDSSEK</u>					
serotype c	<u>KENKVNAPALNVDDKGAKSSEDVNPTVSKTASEVEASAVTATDTKNSNPQVNVETDSNEK</u>					
	190	200	210	220	230	240
serotype f	<u>DENKMVTSAPAKETEAEQNEKAVRENLMQROAKAVSIPSQGNVVFQETTPVKNAASMSSP</u>					
serotype c	<u>DENKMVTSAPAKETEAEQNEKAVAENLMQROAKAVSIPSQGNVVFQETTPVKNAASMSSP</u>					
	250	260	270	280	290	300
serotype f	<u>TOFNEDKDGKVFYDQVLEADGHOWISYVSYSGIRRYAPIAVTIEELKQKEIVQONLPAQG</u>					
serotype c	<u>TOFNEDKDGKVFYDQVLEADGHOWISYVSYSGIRRYAPIAVTIEELKQKEIVQONLPAQG</u>					
	310	320	330	340	350	360
serotype f	<u>TYHFTKQQLK--MKLN-----CLVRPNSRFTTEITFFMIRF-----</u>					
serotype c	<u>TYHFTKQADVNKAELSSPTQFSFYNGDHVFYDKVLEADGHOWISYVSYSGIRRYVVGIG</u>					
	370	380	390	400	410	420
serotype f	-----					
serotype c	<u>LTTQPSPIETKVSGTIAIQNKTAQOQFDVLIISNVSSTOGIKEVLVPVWSEONGODDIVWYQ</u>					
	430	440	450	460	470	480
serotype f	-----					
serotype c	<u>ATKQEGGVYKVTVKVSDHKNNSGNYDIHLYYRLSTGELKVVGKTTVEAPKPVETTGI</u>					
	490	500	510	520	530	540
serotype f	-----					
serotype c	<u>SIANKSSQGFVDLITNASSTOGIKEVLVPVWSEONGODDIWYOATKQEGGVYKVTVKVS</u>					
	550	560	570	580	590	600
serotype f	-----					
serotype c	<u>DHKNDSGNYDIHLYYRLSTGELKVVGKTTTVEAPNRVNLPAQGYVFTNKVEVKNEART</u>					
	610	620	630	640		
serotype f	-----					
serotype c	<u>SSPTQFTFNKGESIIYDSILNADGHOWISYRSYSGIRRYIID</u>					

FIGURE 1B

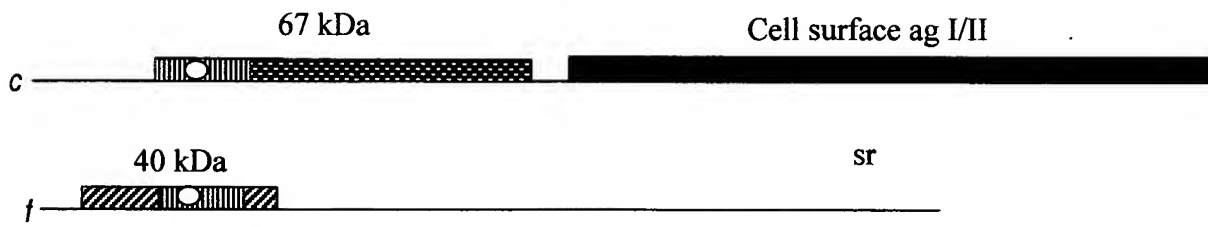


FIGURE 2A

	10	20	30	40
65-1s	VKNAASMSSPTQFNFDKGD	KVFYDKVLEADGHQWISYVS	SYSGIRRY	
40-1s	VKNAASMSSPTQFNFDKGD	KVFYDNVLEADGHQWISYVS	SYSGIRRY	
65-2s	VKNEAKLSSPTQFSFYNGDH	VFYDKVLEADGHQWISYVS	SYSGIRRY	
65-3s	VKNEARTSSPTQFTFNKGES	IYYDSILNADGHQWISYRS	SYSGIRRY	
Bsp-2s	VKNEAKVASPTQFTLDKGD	RIFYDQILTIEGNQWLSYKS	FNGVRRF	
Bsp-3s	--KEAKISSQTQFTLEKGD	KINYDQVLTADGYQWISYKS	SYSGVRRY	
Bsp-4s	VKSQPKVSSPVEFNFQKGE	KIHYDQVLVVDGHQWISYKS	SYSGIRRY	
Bsp-1s	VKNTPSKSAPVAFYAKKGD	KVFYDQVFNKDNVKWISYKS	SFCGVRRY	
	. . . : * . . . : * : * : * : . . . : * : * : * : * : * : *			
SH3b	VRNSPGTSSPIIGTLKKGD	KVKVLGVDG....DWADITY	GSGQRGY	
	* * * * *	* * * * *	* * * * *	

FIGURE 2B

	10	20	30	40	50	60
65-1L	QQFDVLIISNVSSQTQGIKE	VLVPVWSEQNGQDDIVWYQ	ATKQGE	GVYKVT	TVKVS	SDHKNN
65-2L	QGFDVLIITNASSTQGIKE	VLVPVWSEQNGQDDIIWYQ	ATKQGE	GVYKVT	TVKVS	SDHKND
Bsp-L	-GFDILITNIKDDNGIAAVK	VPVWTEQGGQDDIKWYTAV	TTGDG	NYKVA	VSFADH	KNEKG
	** : * : * . . . : * * * * * : * : * * * * * * * * . . . * : * * * * : * . . . : * * * * : *					
	70	80				
65-1L	NYDIHLYYRLSTGELKVVG	GKTTEVEAP				
65-2L	NYDIHLYYRLSTGELKVVG	GKTTEVEAP				
Bsp-L	LYNIHLYYQEASGTLVGV	TGTVAGT				
	* : * * * * * : : * * * * * . . . * . .					

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c -----
f ATAGTAAAAATTTTCAAAAAATATATTACGTAAGTATTGCTAAATATTTCTTTTGTGTTTCAATATAGGTGAAAAAGAAAATGAAGGAAGATTATGAA
    10      20      30      40      50      60      70      80      90     100

c -----1-----ATGAAAAGA
f TCAAAAAATAGTCGTCATTTTCGTCATTTTACATGTTAGGTGCTCATTCTTTCAAAGGCAGTATATCATAATGATAGGAGTGTGAAACTTATGAAAAGA
    110     120     130     140     150     160     170     180     190     200

c 10      20      30      40      50      60      70      80      90     100
f ATTGATATTAATCATCAAGCACAACGTTTTTCTATTTCGCAAAATATGCATTTGGAGCTGCATCTGTTTAAATTGGCTGTGCTTTTTTCTAGGTACCCAAA
    210     220     230     240     250     260     270     280     290     300

c 110     120     130     140     150     160     170     180     190     200
f ATGTTTCTGCACAAGAGCAGGGAACCAATTGCCAGCAAGTGAAAACGCAGTTGTGAACGTGGCTGAAAATTCAGTTGCTATCAGCCAAGCAGTTTCAGA
    310     320     330     340     350     360     370     380     390     400

c 210     220     230     240     250     260     270     280     290     300
f TAAGGCAGCAGCTCAAACAACCTCTAACAGAAACACCCCAAGTTGAAGTTGAGGAGAAGAAAATAAGGTAATGCTCCTGCTTTAAATGTCGATGACAAA
    410     420     430     440     450     460     470     480     490     500

c 310     320     330     340     350     360     370     380     390     400
f GGTGCAAAATCCAAAGAAGATGTGAACCCCTACTGTTTCAAAGACAGCAAGTGAAGTGAAGCTTCTGCAGTAAGTCTACTGATACTAAAAATTCAAATC
    510     520     530     540     550     560     570     580     590     600

c 410     420     430     440     450     460     470     480     490     500
f CACAAGTCAATGTTGAAACTGACTCAAATGAAAAAGACGAAAATAAAATGGTCACCTCGGCTCCAGCTAAGGAGACTGAGGCAGAACAAAATGAGAAAGC
    610     620     630     640     650     660     670     680     690     700

c 510     520     530     540     550     560     570     580     590     600
f GGTAGCAGAAAATCTTATGCAAAGACAAGCTAAGGCTGTCTCAATTCCATCGCAAGGCAATTATGTTTCCAAGAAACAACCTCTGTAAAAATGCAGCC
    710     720     730     740     750     760     770     780     790     800

c 610     620     630     640     650     660     670     680     690     700
f AGTATGTCCAGCCCAACCAATTTAACTTTGATAAAGGAGATAAGGTTTTTATGATAAGGTTTGAAGCGGATGGGCATCAATGGATTAGCTATGTGT
    810     820     830     840     850     860     870     880     890     900

c 710     720     730     740     750     760     770     780     790     800
f CTTACAGTGGTATTCGTCGCTATGCTCCTATTGCTGTGACAATTGAAGAATTGAAGCAAAAAGAAATTGTTTCAGCAAAATTTACCGGCACAAGGAACCTA
    910     920     930     940     950     960     970     980     990    1000

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FIGURE 3

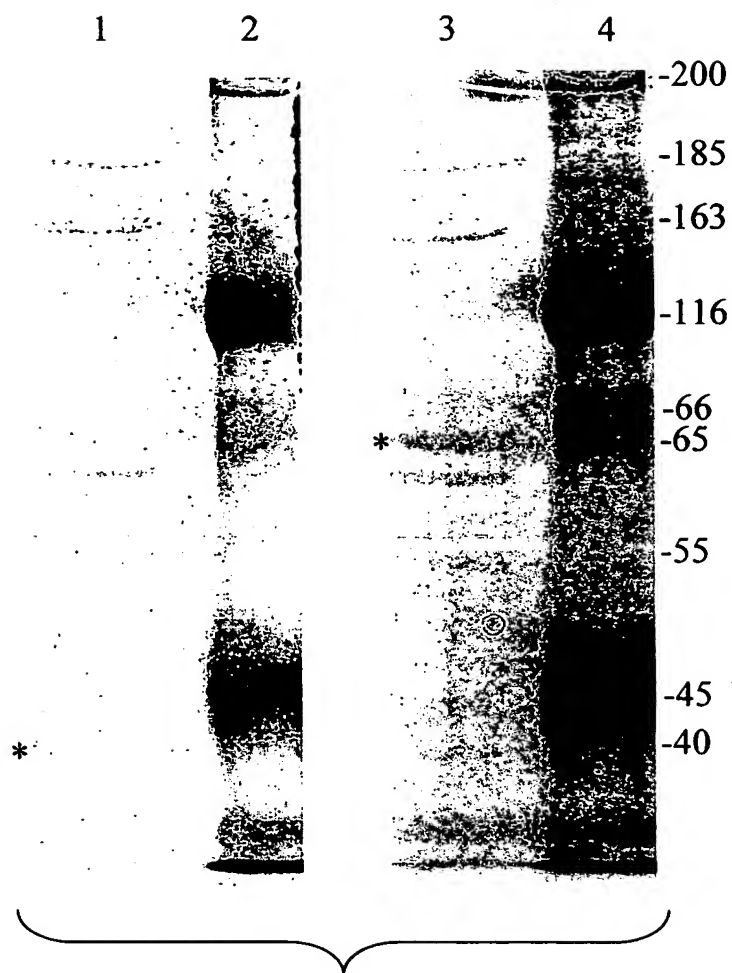


FIGURE 4

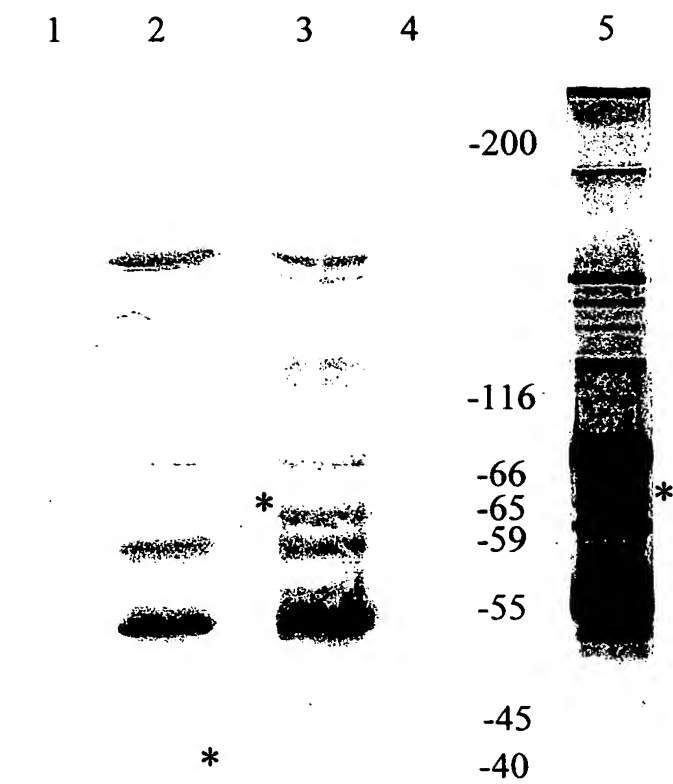


FIGURE 5

Comparison of peptidoglycan source and enzyme source for hydrolytic activity

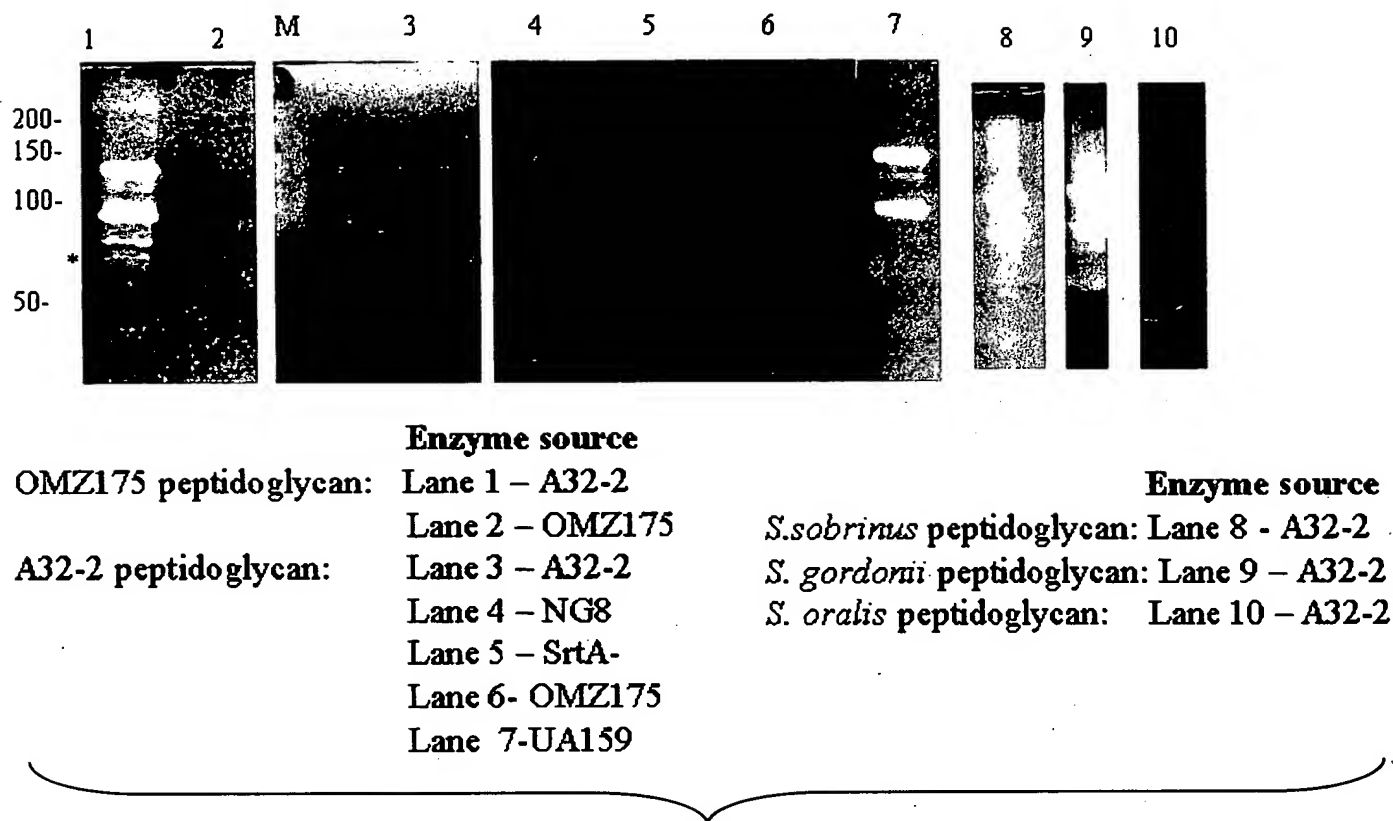
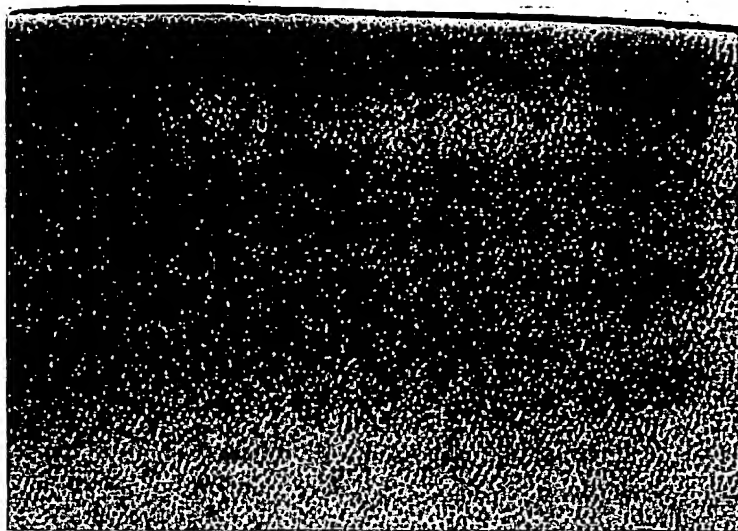


FIGURE 6A

Enzyme source:

NG8 A32-2 Marker



Peptidoglycan source: *Actinobacillus actinomycetemcomitans* 29522

FIGURE 6B

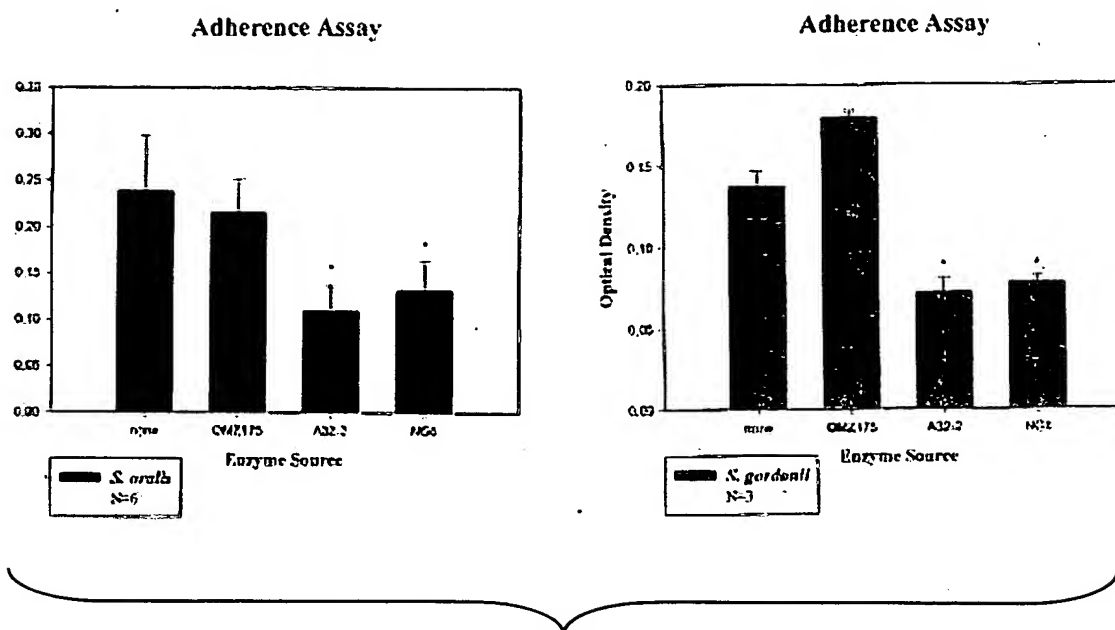


FIGURE 6C

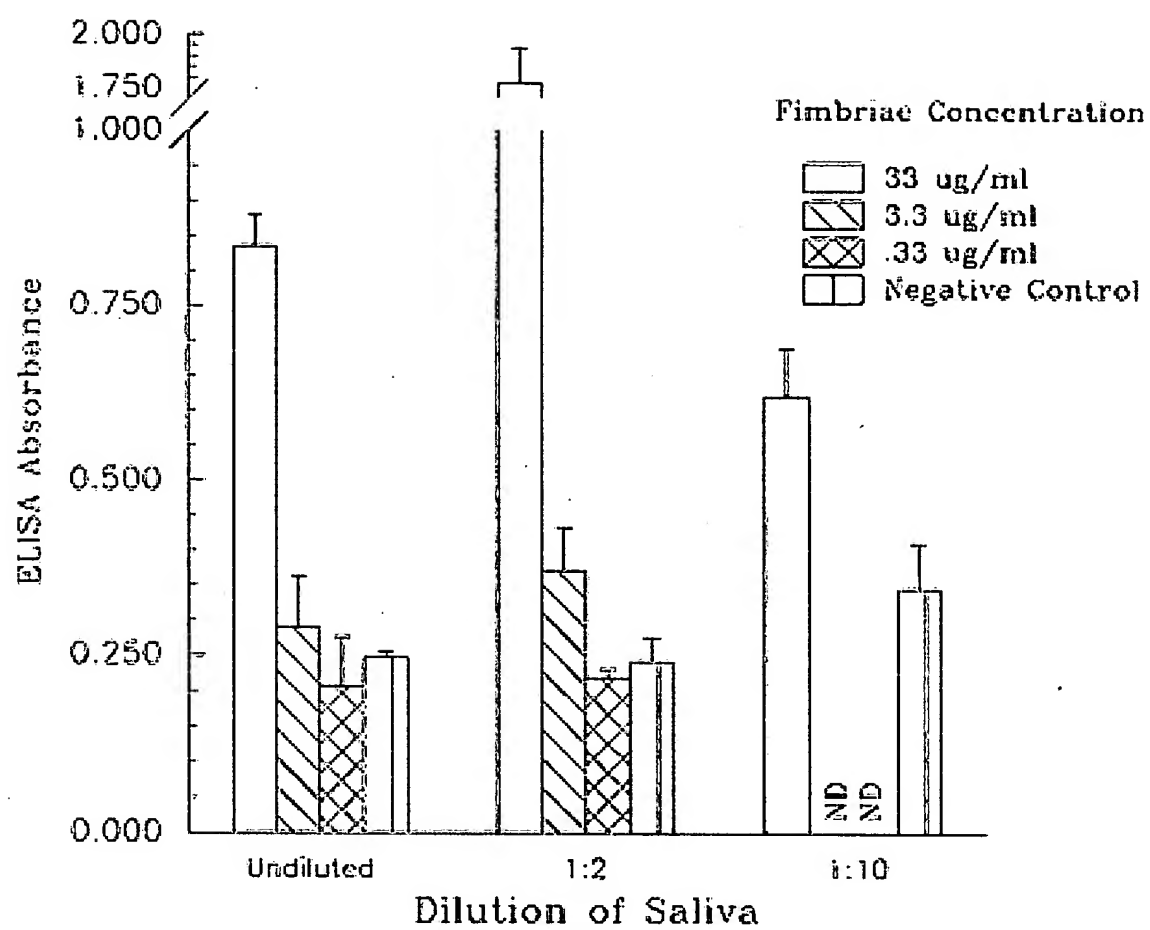


FIGURE 7

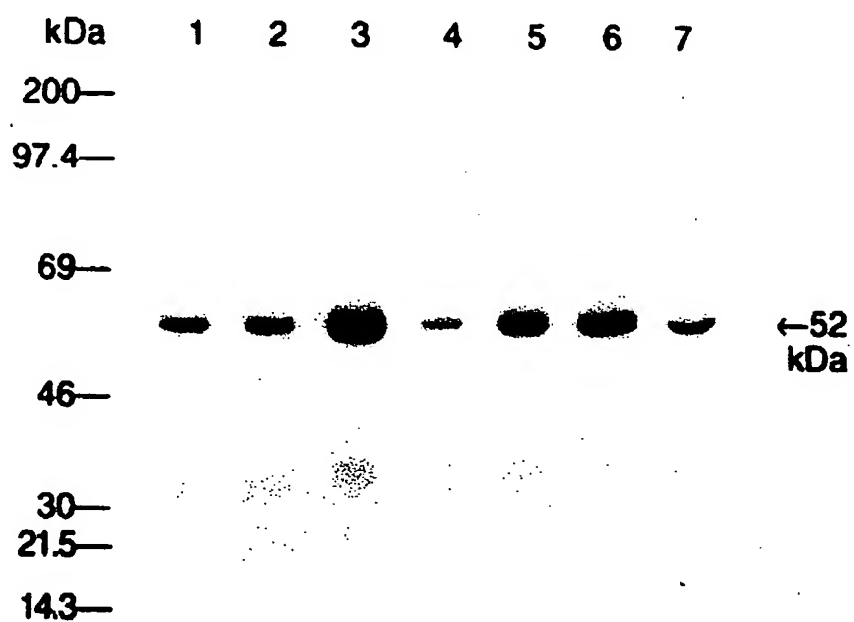


FIGURE 8

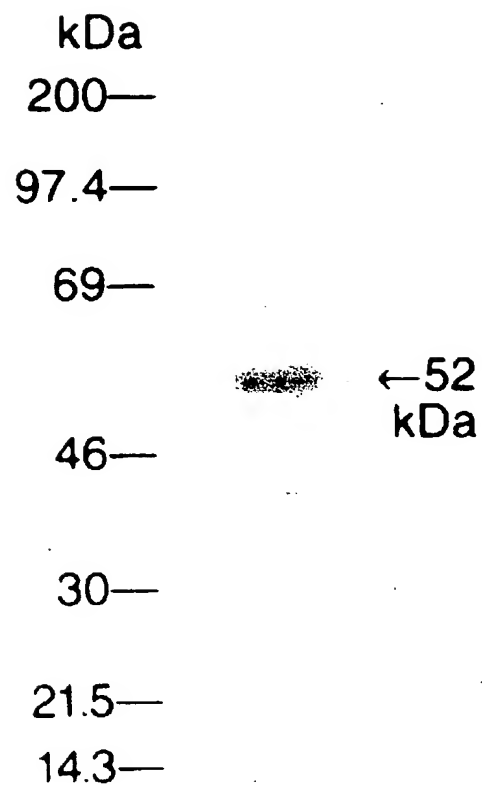


FIGURE 9

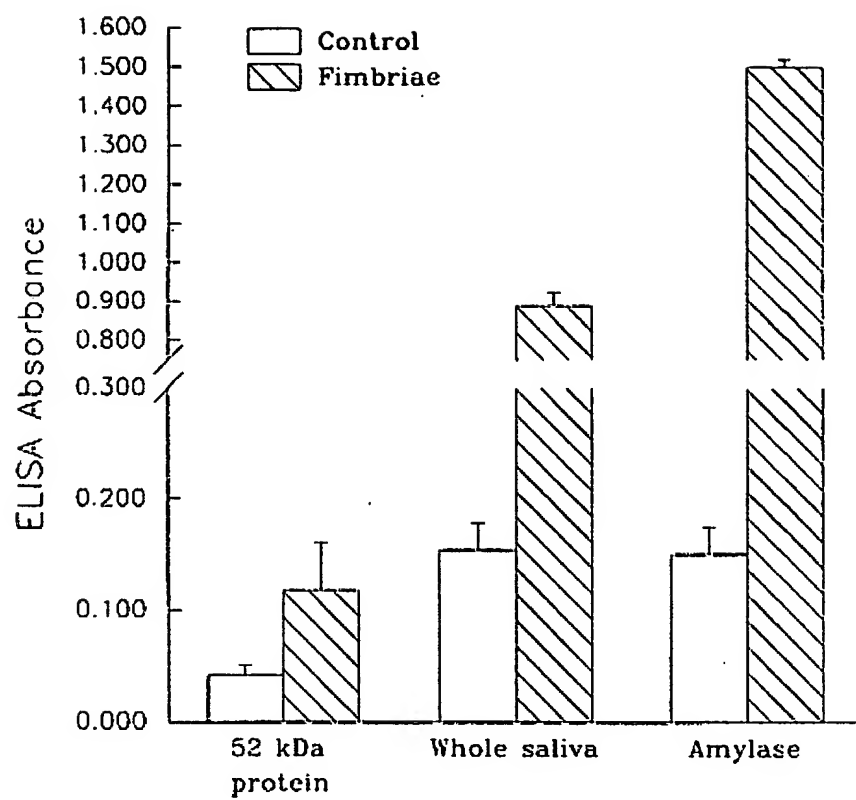


FIGURE 10

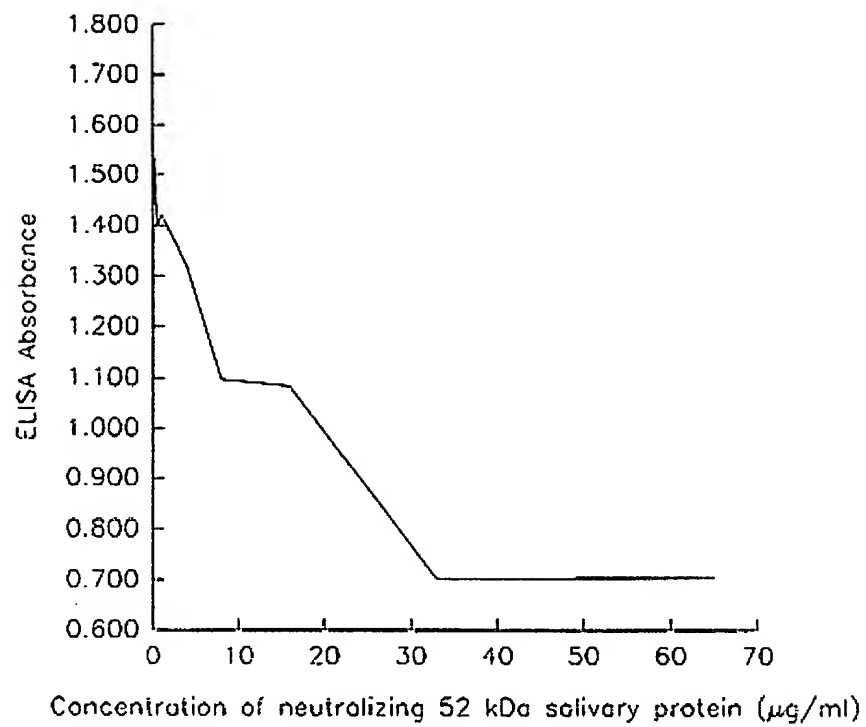


FIGURE 11

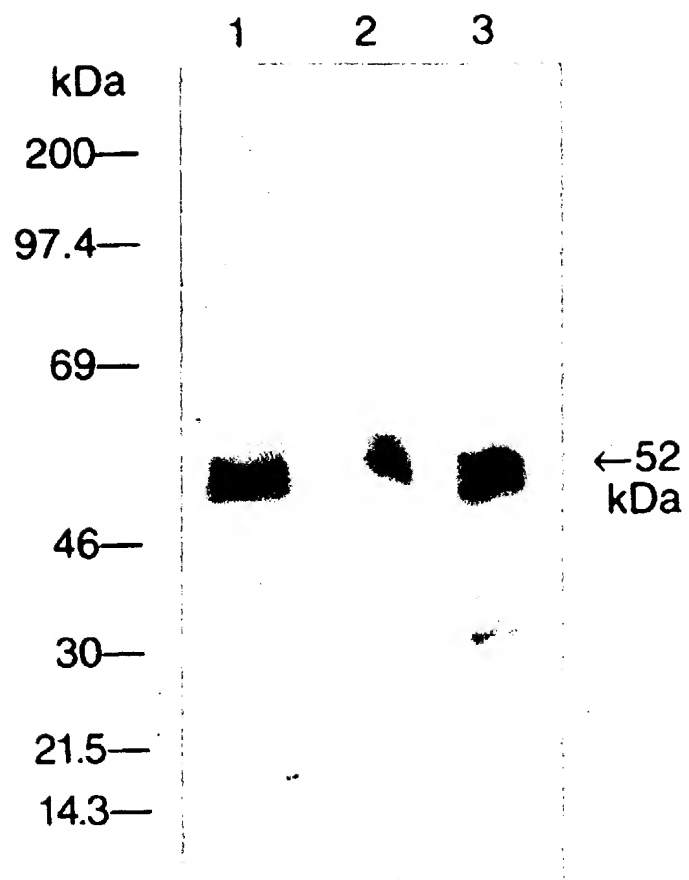


FIGURE 12